

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 15:12:19 ; Search time 147.339 Seconds
(without alignments)
7871.356 Million cell updates/sec

Title: US-09-825-769A-12

Perfect score: 273
Sequence: 1 ccgcgcgtcgtcgtatgacg.....cagcgscgscgscacacgacg 273

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 337863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: N_GeneSeq_29Jan04:*

1: geneseqn19806:*\n2: geneseqn19808:*\n3: geneseqn20008:*\n4: geneseqn2001as:*\n5: geneseqn2001bs:*\n6: geneseqn2002as:*\n7: geneseqn2003as:*\n8: geneseqn2003bs:*\n9: geneseqn2003cs:*\n10: geneseqn2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	272	99.6	273	6	AAAS15486
2	270.4	99.0	1212	6	AAAS15486 B. pertussis
3	189.4	69.4	1212	6	ABO90070 M. capuul
4	153.6	56.3	1215	2	AAZ09786 E. coli b
5	153.6	56.3	1232	2	AAZ02811 E. coli b
6	153.6	56.3	1419	5	AAAS88509 DNA encod
7	153.6	56.3	1548	5	AAAS88547 DNA encod
8	153.6	56.3	1548	5	AAAS93345 DNA encod
9	153.6	56.3	1548	5	AAAS73075 DNA encod
10	153.6	56.3	3414	5	AAAS73033 DNA encod
11	153.6	56.3	3481	2	AAAX02815 DNA encod
12	153.6	56.3	3810	2	AAAX02813 DE1973127
13	153.6	56.3	10614	4	AAAS46259 DNA encod
14	148.8	54.5	1212	7	ABZ39842 N. gonorr
15	140.8	51.6	13786	3	AAAB1480 N. mening
16	140.8	51.6	110000	3	AAAB1480 N. mening
17	140.8	51.6	349980	3	AAAF21610 Neisseria
18	139.4	51.1	425	6	AAAS15487 B. pertussis
19	120.6	44.2	1215	7	ACF72052 Phototab
20	120.6	44.2	110000	7	ACF72052 Phototab
21	120.6	44.2	110000	7	ACF72052 Phototab
22	117.4	43.0	1518	4	ABL09101 Drosophila
23	117.4	43.0	3041	4	ABL11656 Drosophila

24	117.4	43.0	3576	4	ABL09100
25	112	41.0	62909	4	AAAF28545
26	111	40.7	1140	7	ABT18305
27	111	40.7	1140	7	ABT18900
28	111	40.7	1554	7	ABT20720
29	111	40.7	1778	7	ABT20122
30	111	40.7	3140	7	ABT17712
31	111	40.7	3778	7	ABT19526
32	106.2	38.9	1260	8	ADA32431
33	105.8	38.8	565	6	AAAS15485
34	90.8	33.3	110000	2	AAAT42063_03
35	88.8	32.5	1362	6	ABZ12797
36	88.8	32.5	1399	3	AAZ98363
37	88.8	32.5	1494	7	AAAD8348
38	88.8	32.5	1656	3	AAAC42345
39	88.8	32.5	11198	4	AAAD07496
40	88.8	32.5	11201	4	AAAD07498
41	88.8	32.5	11204	4	AAAD07499
42	88.8	32.5	11427	4	AAAD07497
43	88.8	32.5	12008	4	AAAD07500
44	88.8	32.5	12844	4	AAAD07492
45	88.8	32.5	12850	4	AAAD07495

ALIGNMENTS

RESULT 1	AAAS15486 standard; DNA; 273 BP.
ID	AAAS15486;
AC	AAAS15486;
XX	
AC	AAAS15486;
XX	
DT	29-AUG-2003 (revised)
DT	14-FEB-2002 (first entry)
XX	
DE	B. pertussis cysteine desulphinase DNA (DSF536R1) from strain BP536.
XX	
KM	Large-scale bacterial toxin production; pertussis toxin; PT;
KM	whooping cough vaccine; cysteine desulphinase; ds.
XX	
OS	Bordetella pertussis; strain BP536.
XX	
PN	MO200174862-A2.
XX	
PF	04-APR-2001; 2001WO-US010938.
XX	
PR	04-APR-2000; 2000US-0194478P.
XX	
PA	04-APR-2000; 2000US-0194482P.
XX	
PA	(BAXT) BAXTER INT INC.
XX	(BAXT-) BAXTER HEALTHCARE SA.
XX	
PT	Blake MS, Bogdan JA, Nazario-Larrieu J;
XX	WPI; 2002-010777/01.
XX	
PT	Enhancing production of bacterial toxins comprises eliminating or
PT	reducing toxin expression inhibitors formed by toxin producing bacteria
XX	by adding at least one soluble metal salt that forms an insoluble complex
XX	with sulfate.
XX	
PS	Disclosure; Fig 7; 46pp; English.
XX	
CC	The present invention relates to a method of enhancing the production of
CC	bacterial toxins in large-scale cultures. The method comprises
CC	eliminating or reducing toxin expression inhibitors formed by toxin
CC	producing bacteria. The invention provides a method for producing
CC	pertussis toxin (PT) from Bordetella pertussis by introducing a soluble
CC	salt into the growth medium that sequesters sulphate and/or employing a
CC	B. pertussis cysteine desulphinase knockout mutant. The method is useful

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 15:12:19 ; Search time 229.374 Seconds
(without alignments)
7871.356 Million cell updates/sec

Title: US-09-825-769A-11

Perfect score: 425
Sequence: 1 ctcgacctgcagaagctcga.....ggttcgacctgcagctgcgc 425

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: geneseq1980s:*\n2: geneseq1990s:*\n3: geneseq2000s:*\n4: geneseq2001as:*\n5: geneseq2001bs:*\n6: geneseq2002s:*\n7: geneseq2003as:*\n8: geneseq2003bs:*\n9: geneseq2003cs:*\n10: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	425	100.0	425	6	AA515487
2	424	99.8	1212	6	AA515484
3	334	78.6	560	6	AA515488
4	288	67.8	1212	6	ABO90070
5	246.4	58.0	1215	2	AAZ09786
6	246.4	58.0	1232	2	AAK02811
7	246.4	58.0	1548	5	AA88547
8	246.4	58.0	1548	5	AA893345
9	246.4	58.0	1548	5	AA873075
10	246.4	58.0	3414	5	AA573033
11	246.4	58.0	3481	2	AAK02815
12	246.4	58.0	3810	2	AAK02813
13	246.4	58.0	10614	4	AA846259
14	232.6	54.7	1212	7	AB239842
15	213.4	50.2	13786	3	AAA81480
16	213.4	50.2	110000	3	AAA81490
17	213.4	50.2	349980	3	AA821610
18	184	43.3	1215	7	ACF72052
19	184	43.3	110000	7	ACF67367
20	184	43.3	110000	7	ACF65387
21	162	38.1	1419	5	AA88509
22	158.8	37.3	62909	4	AA828545
23	156.8	36.9	1260	8	ADA32431

24	147.2	34.6	1554	7	ABT20720
25	144.8	34.1	110000	2	AA515486
26	139.4	32.8	273	4	AA515487
27	119.2	28.0	1518	4	ABL09101
28	119.2	28.0	3041	4	ABL11656
29	119.2	28.0	3576	4	ABL09100
30	118.4	27.9	1434	9	ADB69794
31	118.4	27.9	40681	6	ABA92787
32	112.8	26.5	1649	3	AA818102
33	112.8	26.5	2380	4	AAH14339
34	112.8	26.5	3224	5	ABV27901
35	109	25.6	1362	6	ABZ12797
36	109	25.6	1399	3	AA298363
37	109	25.6	1656	9	AA842345
38	107	25.2	1653	9	ADB68433
39	107	25.2	3653	9	ADB69072
40	102.4	24.1	2092	4	AAH14100
41	97.2	22.9	1140	7	ABT18306
42	97.2	22.9	1140	7	ABT18900
43	97.2	22.9	3140	7	ABT20122
44	97.2	22.9	3140	7	ABT17712
45	97.2	22.9	3778	7	ABT19526

ALIGNMENTS

RESULT 1
AA515487
ID AA515487 standard; DNA; 425 BP.
XX
AC AA515487;
XX
DT 29-AUG-2003 (revised)
DT 14-FEB-2002 (first entry)
XX
DE B. pertussis cysteine desulphinase DNA (DSF53611) from strain BP536.
XX
KW Large-scale bacterial toxin production; pertussis toxin; PT;
KW whooping cough vaccine; cysteine desulphinase; ds.
XX
OS Bordetella pertussis; strain BP536.
XX
PN W0200174862-A2.
XX
PD 11-OCT-2001.
XX
PF 04-APR-2001; 2001WO-US010938.
XX
PR 04-APR-2000; 2000US-0194478P.
PR 04-APR-2000; 2000US-0194482P.
PA (BAXT) BAXTER INT INC.
PA (BAXT-) BAXTER HEALTHCARE SA.
XX
PI Blake MS, Bogdan JA, Nazario-Larrieu J;
XX WPI; 2002-010777/01.
XX
PT Enhancing production of bacterial toxins comprises eliminating or
PT reducing toxin expression inhibitors formed by toxin producing bacteria
PT by adding at least one soluble metal salt that forms an insoluble complex
PT with sulfate.
XX
PS Disclosure; Fig 7; 46pp; English.
XX
CC The present invention relates to a method of enhancing the production of
CC bacterial toxins in large-scale cultures. The method comprises
CC eliminating or reducing toxin expression inhibitors formed by toxin
CC producing bacteria. The invention provides a method for producing
CC pertussis toxin (PT) from Bordetella pertussis by introducing a soluble
CC salt into the growth medium that sequesters sulphate and/or employing a
CC B. pertussis cysteine desulphinase knockout mutant. The method is useful

score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

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AL646062 RA

AB004799 PB
AE010130 A-

AR016960 PB

AK38 / 886 SE
AR004633 DE

AL0621215 SA
AR016835 SA

AB005483 FB

AL162756 Ne

BD136659 Pr

AX000472 Se

AX000480 Se

AX000476 Se
PD072278 D-

AB015273 Sh
AB000239 Pa

AAJ 70241 SE
D90883 E. CO

AC020881 Mu
AE016987 Sh

AJ279023 CA

AB002486 Ne.

AP006583 G1

AP005333 V11

AP005075 V11

AY138456 Xer

AK072043 Orj

Genome: 14

D., Thomson,

Jey, S.D.,

Result No.	Score	Query Match	Length	DB	ID	Description
1	270.4	99.0	346274	1	BX640443	BX640443 Bordetell
2	270.4	99.0	349354	1	BX640416	BX640416 Bordetell
3	268.8	98.5	344321	1	BX640429	BX640429 Bordetell
4	220.8	80.9	193050	1	AL646062	AL646062 Ralstonia
C 5	208	76.2	301846	1	AE016913	AE016913 Chromobac
C 6	188.8	69.2	14652	1	AB004799	AB004799 Pseudomon
7	184	67.4	7886	1	AF010139	AF010139 Acetobact
8	168	61.5	300861	1	AE016777	AE016777 Pseudomon
9	162.2	59.4	311249	1	AE016860	AE016860 Pseudomon
10	158.4	58.0	1251	6	AR387886	AR387886 Sequence
11	157.4	57.7	10107	1	AE004633	AE004633 Pseudomon
C 12	157.4	57.7	145050	1	AL652725	AL652725 Salmonell
C 13	157.4	57.7	300431	1	AE016835	AE016835 Salmonell
C 14	155.8	57.1	15982	1	AE008815	AE008815 Salmonell
C 15	155.2	56.8	9356	1	AE005483	AE005483 Escherich
C 16	155.2	56.8	270365	1	AP002562	AP002562 Escherich
C 17	155.2	56.8	329861	1	NMA522491	AL162756 Neisseria
18	153.6	56.3	1215	6	AX019664	AX019664 Sequence
19	153.6	56.3	1215	6	BD136659	BD136659 Process f
20	153.6	56.3	1232	6	AX000472	AX000472 Sequence
21	153.6	56.3	1233	6	BD073376	BD073376 Process f
22	153.6	56.3	3481	6	AX000480	AX000480 Sequence
23	153.6	56.3	3481	6	BD073380	BD073380 Process f
24	153.6	56.3	3810	6	AX000476	AX000476 Sequence
25	153.6	56.3	3810	6	BD073378	BD073378 Process f
C 26	153.6	56.3	9329	1	AE015273	AE015273 Shigella
C 27	153.6	56.3	10614	1	AE000339	AE000339 Escherich
C 28	153.6	56.3	10614	1	AX370241	AX370241 Sequence
C 29	153.6	56.3	13332	1	D90883	D90883 E.coli geno
C 30	153.6	56.3	241679	2	AC020861	AC020861 Mus muscu
C 31	153.6	56.3	290380	1	AE016987	AE016987 Shigella
C 32	152	55.7	300099	1	AE016764	AE016764 Escherich
C 33	143	52.4	1450	1	CRU279023	CRU279023 Candida r
C 34	141.4	51.6	308015	1	AE016783	AE016783 Pseudomon
C 35	140.8	51.6	10203	1	AE002486	AE002486 Neisseria
C 36	140.8	51.6	349980	6	AX044032	AX044032 Sequence
C 37	137	50.2	159119	1	AP006583	AP006583 Gloeobact
C 38	135.2	49.5	313518	1	AE016856	AE016856 Pseudomon
C 39	135	49.5	251720	1	AP005333	AP005333 Vibrio vu
C 40	135	49.5	301442	1	AE016798	AE016798 Vibrio vu
C 41	133.4	48.9	301235	1	AP005075	AP005075 Vibrio pa
C 42	130.2	47.7	310029	1	AE016868	AE016868 Pseudomon
C 43	128.6	47.1	6149	1	AY138456	AY138456 Xenorhabd
C 44	128	46.9	1605	8	AK059171	AK059171 Oryza sat
C 45	128	46.9	1816	8	AK072043	AK072043 Oryza sat

AL932800 AL932800-

FEATURES

Location/Qualifiers

FEATURES

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 15:12:20 ; Search time 188.48 Seconds

(without alignments)
9754.272 Million cell updates/sec

Title: US-09-825-769a-11

Perfect score: 425
Sequence: 1 ctcgacccctcagaagctgaa.....ggtcgcctcgcacgtcgcgc 425

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank! :
1: gb_ba :
2: gb_hgt :
3: gb_in :
4: gb_om :
5: gb_ov :
6: gb_pat :
7: gb_ph :
8: gb_pl :
9: gb_pr :
10: gb_ro :
11: gb_sbs :
12: gb_sy :
13: gb_un :
14: gb_vl :
15: em_ba :
16: em_fun :
17: em_hum :
18: em_in :
19: em_mu :
20: em_om :
21: em_or :
22: em_ov :
23: em_pat :
24: em_ph :
25: em_pl :
26: em_ro :
27: em_sbs :
28: em_un :
29: em_vl :
30: em_hgt_hum :
31: em_hgt_inv :
32: em_hgt_other :
33: em_hgt_mus :
34: em_hgt_pin :
35: em_hgt_rnd :
36: em_hgt_mam :
37: em_hgt_vrt :
38: em_sy :
39: em_hgt_hum :
40: em_hgt_mus :
41: em_hgt_other :

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	424	99.8	349354	1	BX640416
2	422.4	99.4	346274	1	BX640443
3	417.6	98.3	344321	1	BX640429
4	329	77.4	193050	1	AL646062
5	302.4	71.2	301846	1	AB016913
6	280	65.9	14652	1	AB004799
7	260.8	61.4	7886	1	AF010139
8	254.4	59.9	1251	6	AK87886
9	248	58.4	9356	1	AE005483
10	248	58.4	270365	1	AP002562
11	248	58.4	311249	1	AE016860
12	246.4	58.0	1215	6	AX018964
13	246.4	58.0	1215	6	BD136659
14	246.4	58.0	1232	6	AX000472
15	246.4	58.0	1233	6	BD073376
16	246.4	58.0	3481	6	AX000480
17	246.4	58.0	3481	6	BD073380
18	246.4	58.0	3810	6	AX000476
19	246.4	58.0	3810	6	BD073378
20	246.4	58.0	10614	1	AE000339
21	246.4	58.0	10614	6	AX370241
22	246.4	58.0	13332	1	D90883
23	246.4	58.0	241679	2	AC020861
24	244.8	57.6	9329	1	AE015273
25	244.8	57.6	290380	1	AE016987
26	243.2	57.2	300099	1	AE016764
27	240	56.5	145050	1	AL627275
28	240	56.5	300431	1	AE016835
29	238.4	56.1	19982	1	AE008815
30	235.2	55.3	300861	1	AE016777
31	227.8	53.6	329861	1	NMA522491
32	213.4	50.2	10203	1	AE002486
33	213.4	50.2	349980	6	AX044032
34	198.4	46.7	13584	1	AE013736
35	198.4	46.7	204050	1	AL414154
36	193.6	45.6	251720	1	AP005333
37	190.4	44.8	301235	1	AP005075
38	188.8	44.4	14261	1	AE004160
39	188.8	44.4	301442	1	AE016798
40	186.2	43.8	11059	1	AE015668
41	185.6	43.7	10107	1	AE004633
42	184	43.3	348505	1	BX571870
43	177.6	41.8	6149	1	AY138456
44	169.6	39.9	308015	1	AE016783
45	165.8	39.0	1450	8	CRU279023

ALIGNMENTS

RESULT 1
LOCUS BX640416
DEFINITION BX640416
ACCESSION BX640416 BX470248
VERSION BX640416.1 GI:33572374
KEYWORDS complete genome.
SOURCE Bacteriella pertussis Tohama I
ORGANISM Bacteriella pertussis Tohama I
REFERENCE 1
AUTHORS Parkhill,J., Sebatia,M., Preston,A., Murphy,L.D., Thomson,N.,
Harris,D.B., Holden,M.T.G., Churcher,C.R., Bentley,S.D.,

Pred. No. is the number of results predicted by chance to have a

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 15:12:20 / Search time 1546.52 Seconds
(without alignments)
8206.421 Million cell updates/sec

Title: US-09-825-769a-11

Perfect score: 425

Sequence: 1 ccgcgcctcgcagagctgaa.....ggctgcgcctgcagctgcgc 425

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estdb:
2: em_estdb:
3: em_estdb:
4: em_estdb:
5: em_estdb:
6: em_estdb:
7: em_estdb:
8: em_estdb:
9: em_estdb:
10: em_estdb:
11: em_estdb:
12: em_estdb:
13: em_estdb:
14: em_estdb:
15: em_estdb:
16: em_estdb:
17: em_estdb:
18: em_estdb:
19: em_estdb:
20: em_estdb:
21: em_estdb:
22: em_estdb:
23: em_estdb:
24: em_estdb:
25: em_estdb:
26: em_estdb:
27: em_estdb:
28: em_estdb:
29: em_estdb:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
C 1	281.6	66.3	853	28	BZ576834
2	280	65.9	1202	28	BZ568162
3	196.8	46.3	904	28	BZ554829
4	155.4	36.6	658	13	BZ672399

Result No.	Score	Query Match	Length DB	ID	Description
5	154.6	36.4	554	14	CF847417
6	152.8	36.0	715	13	BX613550
7	150.2	35.3	1148	28	BZ575496
8	142.2	33.5	806	14	CF402355
9	141.6	33.3	622	10	BE195251
10	137.8	32.4	869	14	CB659834
11	133.6	31.4	457	12	BG333522
12	130.4	30.7	1172	28	BZ585655
13	130.2	30.6	980	11	CNS08MEH
14	128.4	30.2	773	13	BX870153
15	128.2	30.2	1491	11	AX107707
16	126.6	29.8	378	14	W06757
17	125	29.4	614	13	BQ295727
18	124	29.2	2027	11	AK075575
19	123.4	29.0	781	14	CF672802
20	122.4	28.8	734	12	BG864405
21	122.4	28.8	738	12	B1146788
22	122.4	28.8	885	14	CA984300
23	121.4	28.6	728	28	BH593957
24	120.8	28.4	602	9	AL932800
25	119.8	28.2	796	28	BZ435501
26	119	28.0	367	28	CC143041
27	118.6	27.9	798	12	BG970636
28	118.2	27.8	809	12	B1655170
29	117.8	27.7	635	12	BG521402
30	117.2	27.6	607	12	B1247332
31	116.4	27.4	964	28	BZ573485
32	115.2	27.1	304	28	CC142377
33	114.8	27.0	605	10	AM496203
34	114.6	27.0	1925	11	AK005724
35	114.4	26.9	571	10	BES93476
36	114.4	26.9	684	14	CF843243
37	112.8	26.5	649	14	CD671950
38	112.8	26.5	901	13	BQ228630
39	112.8	26.5	963	12	BG105831
40	112.8	26.5	963	14	CF619347
41	111.4	26.2	464	10	AM201019
42	110	25.9	934	13	B1174000
43	109.6	25.8	689	12	BG290339
44	108.6	25.6	668	12	BG848280
45	107.4	25.3	468	29	CG045338

ALIGNMENTS

RESULT 1
LOCUS BZ576834/C 853 bp DNA linear GSS 17-DEC-2002
DEFINITION msh2_5124.y2 msh Pseudomonas aeruginosa genomic clone msh2_5124,
genomic survey sequence.
ACCESSION BZ576834
VERSION BZ576834.1 GI:27211895
KEYWORDS GSS.

SOURCE

ORGANISM

Pseudomonas aeruginosa
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

REFERENCE

AUTHORS

TITLES

JOURNAL

COMMENT

GENOME CENTER

UNIVERSITY OF WASHINGTON

BOX 352145, SEATTLE, WA 98105-2145, USA

TEL: 2062216954

FAX: 2066857244

EMAIL: craymond@u.washington.edu

CLASS: shotgun.

LOCATION/QUALIFIERS

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 15:12:20 / Search time 2488.36 Seconds

(without alignments)
9754.272 Million cell updates/sec

Title: US-09-825-769a-10

Sequence: 1 ggcgcagccgcgcgtgngn.....tcgacgtggcgcgcgactga 560

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

1: Genbank1.*
2: gb_ba.*
3: gb_hcg.*
4: gb_in.*
5: gb_ov.*
6: gb_ov.*
7: gb_ov.*
8: gb_ov.*
9: gb_ov.*
10: gb_ov.*
11: gb_ov.*
12: gb_ov.*
13: gb_ov.*
14: gb_ov.*
15: gb_ov.*
16: gb_ov.*
17: gb_ov.*
18: gb_ov.*
19: gb_ov.*
20: gb_ov.*
21: gb_ov.*
22: gb_ov.*
23: gb_ov.*
24: gb_ov.*
25: gb_ov.*
26: gb_ov.*
27: gb_ov.*
28: gb_ov.*
29: gb_ov.*
30: gb_ov.*
31: gb_ov.*
32: gb_ov.*
33: gb_ov.*
34: gb_ov.*
35: gb_ov.*
36: gb_ov.*
37: gb_ov.*
38: gb_ov.*
39: gb_ov.*
40: gb_ov.*
41: gb_ov.*

```

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	99.3	349354	1	BX640416
2	552.8	98.7	345274	1	BX640443
3	548	97.9	344321	1	BX640429
4	396	70.7	193050	1	AL646062
5	386.4	69.0	301846	1	AE016913
6	325.6	58.1	14652	1	AE004799
7	308	55.0	7886	1	AF010139
8	300	53.6	1215	6	AX018964
9	300	53.6	1215	6	BD136659
10	300	53.6	1233	6	BD073376
11	300	53.6	1251	6	AR387886
12	300	53.6	3481	6	AX000480
13	300	53.6	3481	6	BD073380
14	300	53.6	3810	6	AX000476
15	300	53.6	3810	6	BD073378
16	300	53.6	9356	1	AE005483
17	300	53.6	10614	1	AE000339
18	300	53.6	10614	6	AX370241
19	300	53.6	11332	1	D90883
20	300	53.6	241679	2	AC020861
21	300	53.6	270365	1	AP002562
22	299.6	53.5	1232	6	AX000472
23	298.4	53.3	300099	1	AE016764
24	296.8	53.0	9329	1	AE015273
25	296.8	53.0	290380	1	AE015987
26	290.4	51.9	10203	1	AE02486
27	290.4	51.9	311249	1	AE016860
28	289.4	51.9	349980	6	AX044032
29	288.8	51.6	145050	1	AL627275
30	288.8	51.6	300431	1	NMA52421
31	288.8	51.6	329861	1	AE008815
32	287.2	51.3	19982	1	AE016777
33	279.2	49.9	300861	1	AE004160
34	252	45.0	14261	1	AE013736
35	248.8	44.4	11059	1	AE015668
36	248.8	44.4	13584	1	AE013736
37	248.8	44.4	204050	1	AJ414154
38	247.2	44.1	251720	1	AP005333
39	240.8	43.0	301235	1	AP005075
40	240.8	43.0	301442	1	AE016798
41	240.8	43.0	348505	1	BX571870
42	220	39.3	6149	1	AY138456
43	220	39.3	10507	1	U32721
44	220	39.3	11223	1	AE006068
45	220	39.3	110000	6	AR274513_03

ALIGNMENTS

RESULT 1
LOCUS BX640416
DEFINITION Bordetella pertussis strain Tohama I, complete genome; segment 6/12.
ACCESSION BX640416 BX470248
VERSION BX640416.1 GI:33572374
KEYWORDS complete genome.
SOURCE Bordetella pertussis Tohama I
ORGANISM Bordetella pertussis Tohama I
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Bordetella.

REFERENCE
AUTHORS Parkhill, J., Sebatian, M., Preston, A., Murphy, L.D., Thomson, N., Harris, D.B., Holden, M.T.G., Churcher, C.R., Bentley, S.D.,

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OW nucleic - nucleic search, using sw model

Run on: September 20, 2004, 15:12:19 ; Search time 302.234 Seconds
(without alignments)
7871.356 Million cell updates/sec

Title: US-09-825-769A-10

Perfect score: 560
Sequence: 1 ggcgcagccgcgcgcgtggn.....tcgacgtggccgcgcactga 560

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: N_Geneseq_29Jan04:*

1: geneseqn19808:.*
2: geneseqn19808:.*
3: geneseqn20008:.*
4: geneseqn20018a:.*
5: geneseqn20018b:.*
6: geneseqn20028:.*
7: geneseqn20038a:.*
8: geneseqn20038b:.*
9: geneseqn20038c:.*
10: geneseqn20048:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	99.3	560	AA515488	AA515488 B. pertussis
2	556	99.3	1212	AA515484	AA515484 DNA encod
3	353.4	63.1	1212	ABQ90070	ABQ90070 M. capsul
4	334	59.6	425	AA515487	AA515487 B. pertussis
5	308.8	55.1	1212	AB239842	AB239842 N. gonorr
6	300	53.6	1215	AA209786	AA209786 E. coli b
7	300	53.6	3481	AA209786	AA209786 E. coli b
8	300	53.6	3810	AA209786	AA209786 E. coli b
9	300	53.6	10614	AA546259	AA546259 DNA encod
10	299.6	53.5	1232	AA546259	AA546259 DNA encod
11	290.4	51.9	13786	AA546259	AA546259 DNA encod
12	290.4	51.9	110000	AA546259	AA546259 DNA encod
13	290.4	51.9	110000	AA546259	AA546259 DNA encod
14	254.2	45.4	3414	AA546259	AA546259 DNA encod
15	240.8	43.0	1215	AA546259	AA546259 DNA encod
16	240.8	43.0	110000	AA546259	AA546259 DNA encod
17	240.8	43.0	110000	AA546259	AA546259 DNA encod
18	220	39.3	110000	AA546259	AA546259 DNA encod
19	213.6	38.1	62909	AA546259	AA546259 DNA encod
20	205	36.6	1548	AA546259	AA546259 DNA encod
21	205	36.6	1548	AA546259	AA546259 DNA encod
22	205	36.6	1548	AA546259	AA546259 DNA encod
23	202.4	36.1	1260	AA546259	AA546259 DNA encod

24	192.6	34.4	710	7	ACF66682	ACF66682 Photocorb
25	187.6	33.5	1554	7	ABT20720	ABT20720 Aspergill
26	184.6	33.0	1518	4	ABT09101	ABT09101 Drosophi
27	184.6	33.0	1518	4	ABT11656	ABT11656 Drosophi
28	184.6	33.0	1518	4	ABT09100	ABT09100 Drosophi
29	173	30.9	1649	3	AA518102	AA518102 Lung can
30	173	30.9	2380	4	AA514339	AA514339 Human CD
31	173	30.9	2380	5	ABV27901	ABV27901 Human pro
32	170.8	30.5	1434	9	ADB69794	ADB69794 C. neofor
33	162.6	29.0	2052	4	AAH14100	AAH14100 Human CD
34	149.4	26.7	1362	6	AB212797	AB212797 Arabidops
35	149.4	26.7	1399	3	AA298363	AA298363 A. thalia
36	149.4	26.7	1656	3	AA542345	AA542345 Arabidops
37	142.6	25.5	485	6	ABT80979	ABT80979 Human ova
38	140.2	25.0	40681	6	ABA52787_6	ABA52787_6 Continuation (7 of
39	137	24.5	1778	7	ABT20122	ABT20122 Aspergill
40	137	24.5	3140	7	ABT17712	ABT17712 Aspergill
41	137	24.5	3778	7	ABT19526	ABT19526 Aspergill
42	127.4	22.8	1494	7	AA548348	AA548348 Saccharom
43	127.4	22.8	11198	4	AA547496	AA547496 PYR110P
44	127.4	22.8	11201	4	AA547498	AA547498 PYR107P
45	127.4	22.8	11204	4	AA547499	AA547499 PZB01P DN

ALIGNMENTS

RESULT 1	AA515488	standard; DNA; 560 BP.
ID	AA515488	
XX	AA515488	
AC	AA515488	
XX	AA515488	
DT	29-AUG-2003 (revised)	
DT	14-FEB-2002 (first entry)	
XX		
DE	B. pertussis cysteine desulphinase DNA (DSF53612) from strain BP536.	
XX		
KW	large-scale bacterial toxin production; pertussis toxin; PT;	
KW	whooping cough vaccine; cysteine desulphinase; ds.	
XX		
OS	Bordetella pertussis; strain BP536.	
XX		
PN	W0200174862-A2.	
XX		
PD	11-OCT-2001.	
XX		
PF	04-APR-2001; 2001WO-US010938.	
XX		
PR	04-APR-2000; 2000US-0194478P.	
XX		
PA	04-APR-2000; 2000US-0194482P.	
XX		
XX	(BAXT) BAXTER INT INC.	
XX	(BAXT-) BAXTER HEALTHCARE SA.	
XX		
XX	Blake MS, Bogdan JA, Nazario-Larrieu J,	
XX	WPI; 2002-010777/01.	
XX		
PT	Enhancing production of bacterial toxins comprises eliminating or	
PT	reducing toxin expression inhibitors formed by toxin producing bacteria	
PT	by adding at least one soluble metal salt that forms an insoluble complex	
PT	with sulfate.	
XX		
PS	Disclosure; Fig 7; 46pp; English.	
XX		
CC	The present invention relates to a method of enhancing the production of	
CC	bacterial toxins in large-scale cultures. The method comprises	
CC	eliminating or reducing toxin expression inhibitors formed by toxin	
CC	producing bacteria. The invention provides a method for producing	
CC	pertussis toxin (PT) from Bordetella pertussis by introducing a soluble	
CC	salt into the growth medium that sequesters sulphate and/or employing a	
CC	B. pertussis cysteine desulphinase knockout mutant. The method is useful	

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OM nucleic - nucleic search, using sw model

Run on: September 20, 2004, 15:12:20 ; Search time 2055.97 Seconds

(without alignments)
8206.421 Million cell updates/sec

Title: US-09-825-769a-9

Sequence: 1 atgagacatgcgcacatcra.....ccaaagcaagtcgcagatcc 565

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST:*
1: em_estdb:*
2: em_estdb:*
3: em_estdb:*
4: em_estdb:*
5: em_estdb:*
6: em_estdb:*
7: em_estdb:*
8: em_estdb:*
9: gb_estdb:*
10: gb_estdb:*
11: gb_estdb:*
12: gb_estdb:*
13: gb_estdb:*
14: gb_estdb:*
15: em_estdb:*
16: em_estdb:*
17: em_estdb:*
18: em_estdb:*
19: em_estdb:*
20: em_estdb:*
21: em_estdb:*
22: em_estdb:*
23: em_estdb:*
24: em_estdb:*
25: em_estdb:*
26: em_estdb:*
27: em_estdb:*
28: gb_estdb:*
29: gb_estdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	284	50.3	876	28	BZ577360 mah2_5370
C 2	265.8	47.0	863	28	BZ562611 pac82-164
C 3	245	43.4	1071	28	BZ564477 pac82-164
C 4	233.2	41.3	674	13	CA071128 SCCCAM100

5	233.2	41.3	692	13	CA071140 SCCCAM100
6	225.2	39.9	795	14	CB672482 OSCNBE06T
7	221.4	39.2	655	14	CA186285
8	214.2	37.9	695	9	AU161333
9	214.2	37.9	862	13	BX466420 BX466420
10	212	37.5	668	13	BQ840710 BHE4202 F
11	211.6	37.5	474	13	CA012321 HT05B16T
12	210.2	37.2	673	12	BI997818 101052A1
13	208.8	37.0	651	13	BK624227 BK624227
14	208.2	36.8	941	11	CNS08MEG
15	206.4	36.5	759	13	BK627075 BK627075
16	205	36.3	742	10	BF496153 AU09871.5
17	205	36.3	746	9	A1516894 GH27486.5
18	201.2	35.6	1491	11	AY107707 ZGA maye
19	200.4	35.5	628	13	BX767041 BX767041
20	199	35.2	690	13	BX622505 BX622505
21	197.4	34.9	585	14	CA214446 SCUTP1105
22	196.6	34.8	655	14	CD036744 MGN011XD
23	196.4	34.8	612	9	AU091715 AU091715
24	194.6	34.4	653	12	BI142155 SD16161.5
25	193	34.2	654	13	BU122793 603148834
26	192.2	34.0	864	14	CF377821 AGNCNCURT
27	187.6	33.2	434	9	AU093662 AU093662
28	184.6	32.7	739	14	CF285833 AGNCNCURT
29	184.4	32.6	682	9	AJ456871 AJ456871
30	184.2	32.6	647	12	BU612099 BU612099
31	184.2	32.6	917	13	BU175049 AGNCNCURT
32	183.4	32.5	725	14	CF450610 EST686955
33	183.2	32.4	633	14	CB577181 AMGNVC:N
34	178.6	31.6	744	12	BI330589 BI330589
35	178.6	31.6	750	12	BI854562 603380275
36	178.6	31.6	803	10	BF608290 M11_00123
37	178.6	31.6	829	14	CF837753 UCRCS03_0
38	178.6	31.6	854	14	CF586180 AGNCNCURT
39	178.6	31.6	864	12	BI831420 603074521
40	178.4	31.6	774	12	BI763016 603047806
41	178.4	31.6	876	12	BI824722 603033891
42	178.4	31.6	1018	12	BM452489 AGNCNCURT
43	178.4	31.6	1028	13	BQ073152 AGNCNCURT
44	178.4	31.6	1080	12	BM808412 AGNCNCURT
45	178.4	31.6	1134	12	BM546535 AGNCNCURT

ALIGNMENTS

RESULT 1
LOCUS BZ577360 876 bp DNA linear GSS 17-DEC-2002
DEFINITION mah2_5370.y2 mah Pseudomonas aeruginosa genomic clone mah2_5370,
genomic survey sequence.
ACCESSION BZ577360
VERSION BZ577360.1 GI:27212421
KEYWORDS GSS.
SOURCE Pseudomonas aeruginosa
ORGANISM Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.

REFERENCE
AUTHORS Spencer, D.H., Raymond, C.K., Smith, E.B., Sims, E.B., Haefliger, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
TITLE Whole-Genome-Sequence Variation among Multiple Isolates of
Pseudomonas aeruginosa
JOURNAL J. Bacteriol. (2002) In press
COMMENT Contact: Chris K. Raymond
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Class: Shotgun.
Location/Qualifiers

FEATURES

1	565	100.0	565	6	AA815485	AA815485 B. pertussis
2	539.8	95.5	1212	6	AA815484	AA815484 DNA encod
3	305	54.0	1212	6	AB090070	AB090070 M. capsul
4	275.2	48.7	1212	7	AB239842	AB239842 N. gonorr
5	260	46.0	13786	3	AA81480	AA81480 N. mening
6	260	46.0	110000	3	AA81490_13	Continuation (14 c
7	260	46.0	349980	3	AA81610	AA81610 Neisseria
8	250	44.2	1215	2	AA209786	Aa209786 E. coli b
9	250	44.2	1232	2	AA020811	AA020811 E. coli b
10	250	44.2	3441	5	AA873033	AA873033 DNA encod
11	250	44.2	3481	2	AA820815	AA820815 DB1973127
12	250	44.2	3810	2	AA820813	AA820813 DB1973127
13	250	44.2	10614	2	AA846259	AA846259 DNA encod
14	209	37.0	1215	7	ACF72052	ACF72052 Photobact
15	209	37.0	110000	7	ACF67367_52	Continuation (53 c
16	209	37.0	110000	7	ACF65387_4	Continuation (5 of c
17	205	36.3	1518	4	AB109101	AB109101 Drosophi
18	205	36.3	3576	4	AB109100	AB109100 Drosophi
19	197	34.9	1434	9	ADB69794	ADB69794 C. neofo
20	197	34.9	1653	9	ADB69433	ADB69433 C. neofo
21	197	34.9	3653	9	ADB69072	ADB69072 C. neofo
22	182.6	32.3	1419	5	AA888509	AA888509 DNA encod
23	178.4	31.6	2052	4	AAH14100	AAH14100 Human CDN

24	178.4	31.6	2380	4	AaH14339	AaH14339 Human cDN
25	178.4	31.6	2324	5	ABV27901	ABV27901 Human pro
C 26	176.8	31.3	110000	2	AaT42063_03	Continuation (4 05
27	170.4	30.2	863	4	AaH05422	AaH05422 Human cDN
28	170.2	30.1	1140	7	ABT18306	ABT18306 Aspergill
29	170.2	30.1	1140	7	ABT18900	ABT18900 Aspergill
30	170.2	30.1	1554	7	ABT20720	ABT20720 Aspergill
31	170.2	30.1	1778	7	ABT20122	ABT20122 Aspergill
32	170.2	30.1	3140	7	ABT17712	ABT17712 Aspergill
33	170.2	30.1	3778	7	ABT19526	ABT19526 Aspergill
34	169.8	30.1	1260	8	ADA32431	ADA32431 DNA encod
35	169.6	30.0	62909	5	AAZ28545	AAZ28545 Genomic E
36	156.6	27.7	1362	6	ABZ12797	ABZ12797 Arabidops
37	156.6	27.7	1399	3	AAZ98863	AAZ98863 A. thalia
38	156.6	27.7	1556	3	AAZ42345	AAZ42345 Arabidops
39	155.8	27.6	1194	7	AAD48348	AAD48348 Saccharom
C 40	155.8	27.6	11198	4	AAD07496	AAD07496 PYLR110P
C 41	155.8	27.6	11201	4	AAD07498	AAD07498 PYLR107P
C 42	155.8	27.6	11204	4	AAD07499	AAD07499 PZELP DN
C 43	155.8	27.6	11427	4	AAD07497	AAD07497 PYR251AR
C 44	155.8	27.6	12008	4	AAD07500	AAD07500 PYR1BP DN
C 45	155.8	27.6	12844	4	AAD07492	AAD07492 PYLR110P+

RESULT 1
 AAS15485
 ID AAS15485 standard; DNA; 565 BP.
 XX
 AC AAS15485;
 XX
 DT 29-AUG-2003 (revised)
 DT 14-FEB-2002 (first entry)
 DE B. pertussis cysteine desulphinase DNA (DSF536f1) from strain BP536.
 XX
 KM Large-scale bacterial toxin production; pertussis toxin; PT;
 XX whooping cough vaccine; cysteine desulphinase; ds.
 XX
 OS Bordetella pertussis; strain BP536.
 PN WO200174862-A2.
 PD 11-OCT-2001.
 XX
 PF 04-APR-2001; 2001WO-US010938.
 PR 04-APR-2000; 2000US-0194478P.
 PR 04-APR-2000; 2000US-0194482P.
 PA (BAXT) BAXTER INT INC.
 PA (BAXT-) BAXTER HEALTHCARE SA.
 PI Blake MS, Bogdan JA, Nazario-Larrieu J;
 PI WPI; 2002-010777/01.
 DR
 PT Enhancing production of bacterial toxins comprises eliminating or
 PT reducing toxin expression inhibitors formed by toxin producing bacteria
 PT by adding at least one soluble metal salt that forms an insoluble complex
 PT with sulfate.
 XX
 PS Disclosure; Fig 7; 46pp; English.
 XX
 XX The present invention relates to a method of enhancing the production of
 CC bacterial toxins in large-scale cultures. The method comprises
 CC eliminating or reducing toxin expression inhibitors formed by toxin
 CC producing bacteria. The invention provides a method for producing
 CC pertussis toxin (PT) from Bordetella pertussis by introducing a soluble
 CC salt into the growth medium that sequesters sulphate and/or employing a
 CC B. pertussis cysteine desulphinase knockout mutant. The method is useful